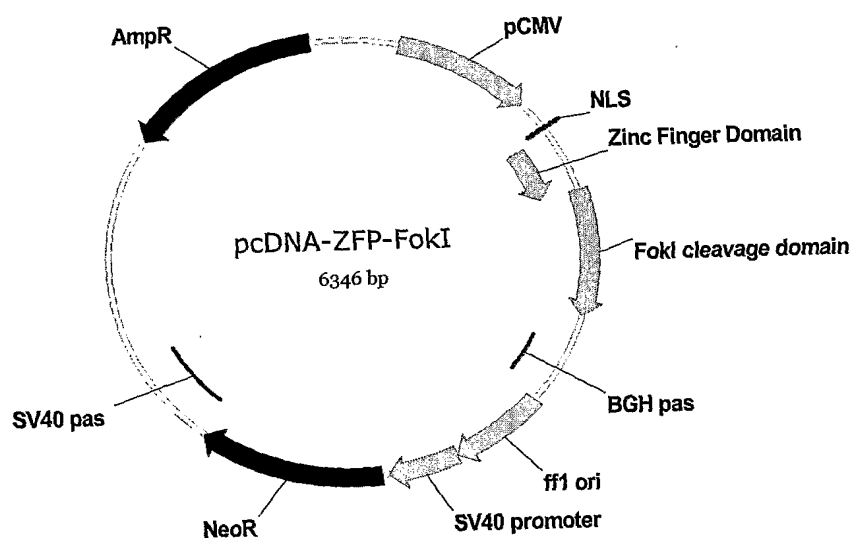
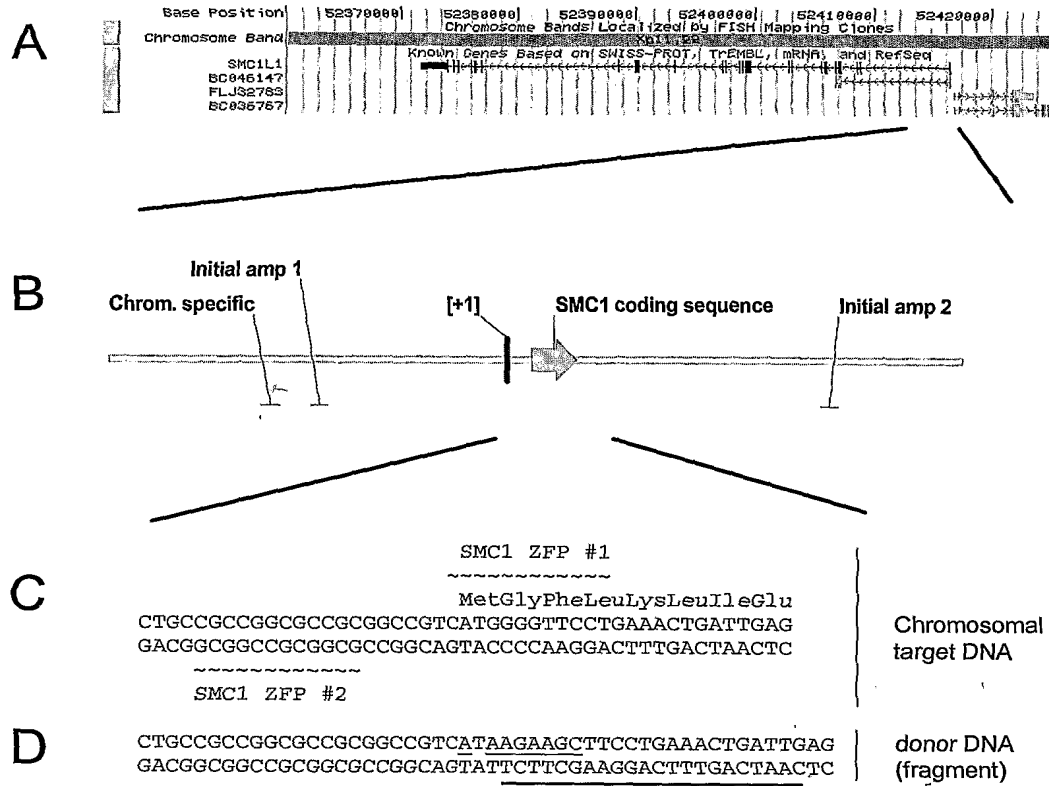


# FIGURE 1

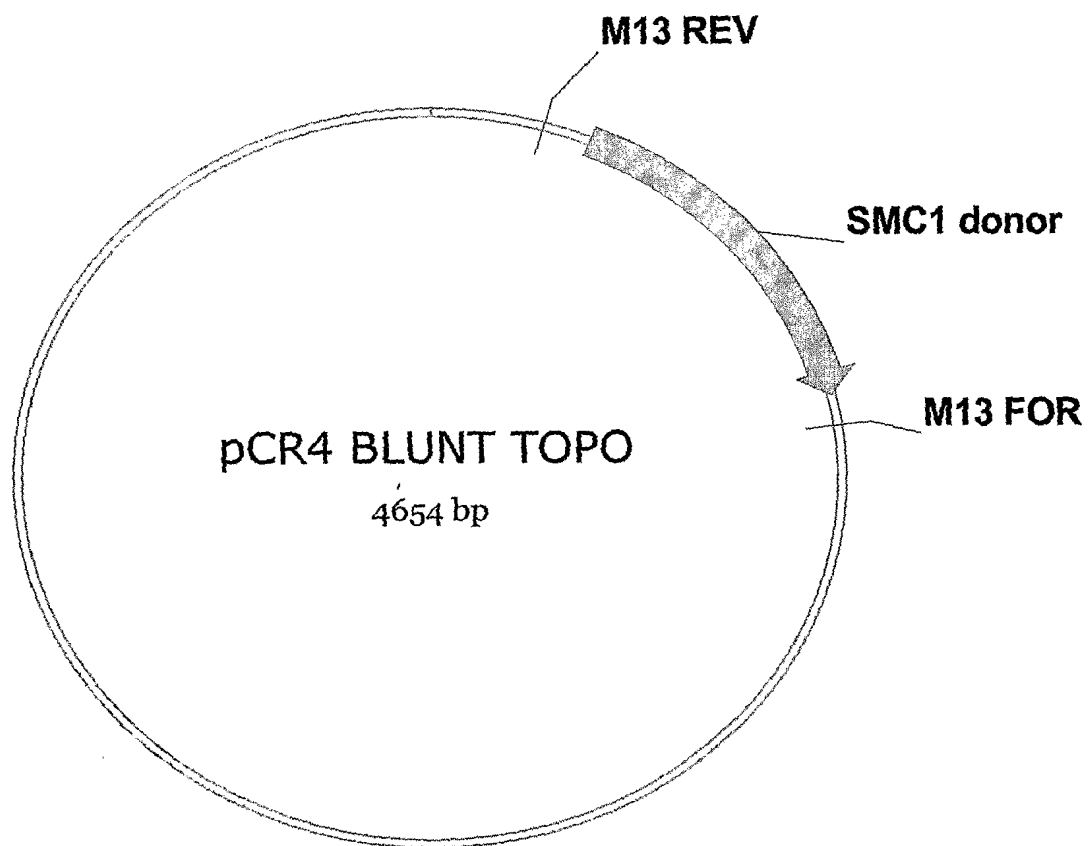
MetGlyPheLeuLysLeuIle (SEQ ID NO:2)  
 CTGCCGCCGGCGCCGCGGCCGTCATGGGGTTCTTGAAGCTGATT  
 GACGGCGCGCCGCGGCCGCGCAGTACCCCAAGGACTTTGACTAA (SEQ ID NO:1)  
 5 10 15 20 25 30 35 40

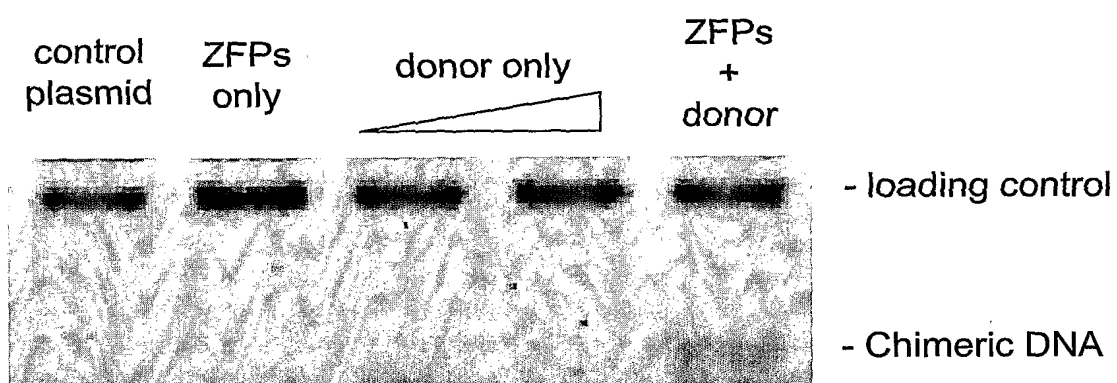
**FIGURE 2**

## FIGURE 3



## FIGURE 4



**FIGURE 5**

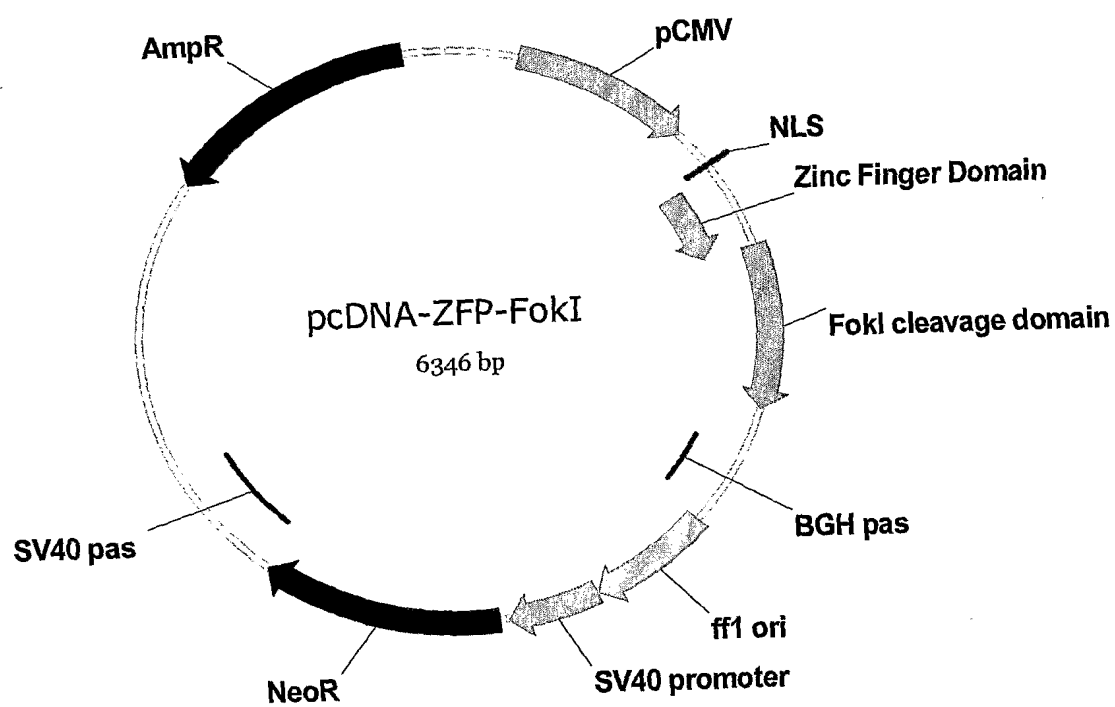
**FIGURE 6**

<u>TAGTCCTGCAGGTTTAAACGAATTCGCCCTTCTCAGCAAGCGTGAGCTCA</u>	50
<u>GGTCTCCCCCGCCTCCTTGAACCTCAAGAACTGCTCTGACTCCGCCCAGC</u>	100
<u>AACAACCTCCTCCGGGGATCTGGTCCGCAGGAGCAAGTGTTTGTTGTTGCC</u>	150
<u>ATGCAACAAGAAAAGGGGGCGGAGGCACCACGCCAGTCGTCAGCTCGCTC</u>	200
<u>CTCGTATACGCAACATCAGTCCCCGCCCCCTGGTCCCACCTCCTGCCGGAAG</u>	250
<u>GCGAAGATCCCGTTAGGCCTGGACGTATTCTCGCGACATTTGCCGGTCGC</u>	300
<u>CCGGCTTGCACTGCGGCGTTTCCC GCGCGGGCTACCTCAGTTCTCGGGCG</u>	350
<u>TACGGCGCGGCCTGTCCTACTGCTGCCGGCGCCGCGGCCGTCATaagaag</u>	400
<u>cTTTCCTGAAACTGATTGAAGGGCGAATTCGCGGCCGCTAAATTCAATTCTG</u>	450
<u>CCCTATAGTGAGT</u>	

(SEQ ID NO: 6)

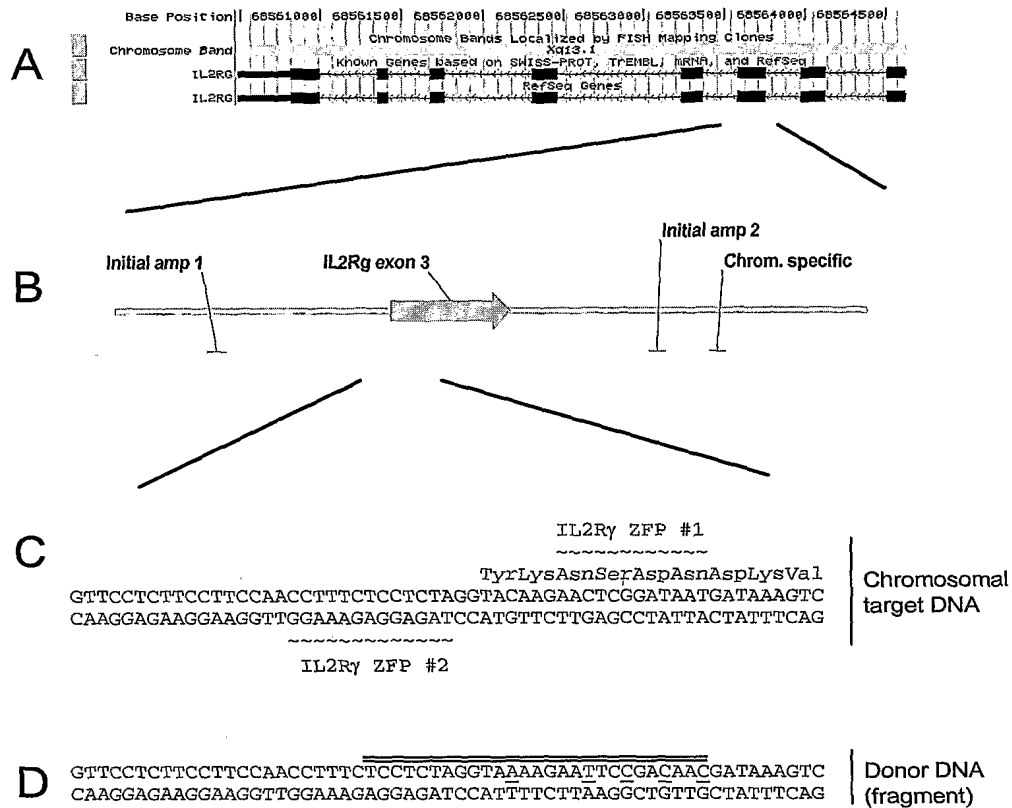
### FIGURE 7

TyrLysAsnSerAspAsnAspLysVal (SEQ ID  
 NO:8)  
 CTTCCAACCTTTCTCCTCTAGGTACAAGAACTCGGATAATGATAAAGTCC  
 GAAGGTTGGAAGAGGAGATCCATGTTCTTGAGCCTATTACTATTTCAGG (SEQ ID  
 NO:7)  
 | | | | | | | | | |  
 5 10 15 20 25 30 35 40 45 50

**FIGURE 8**

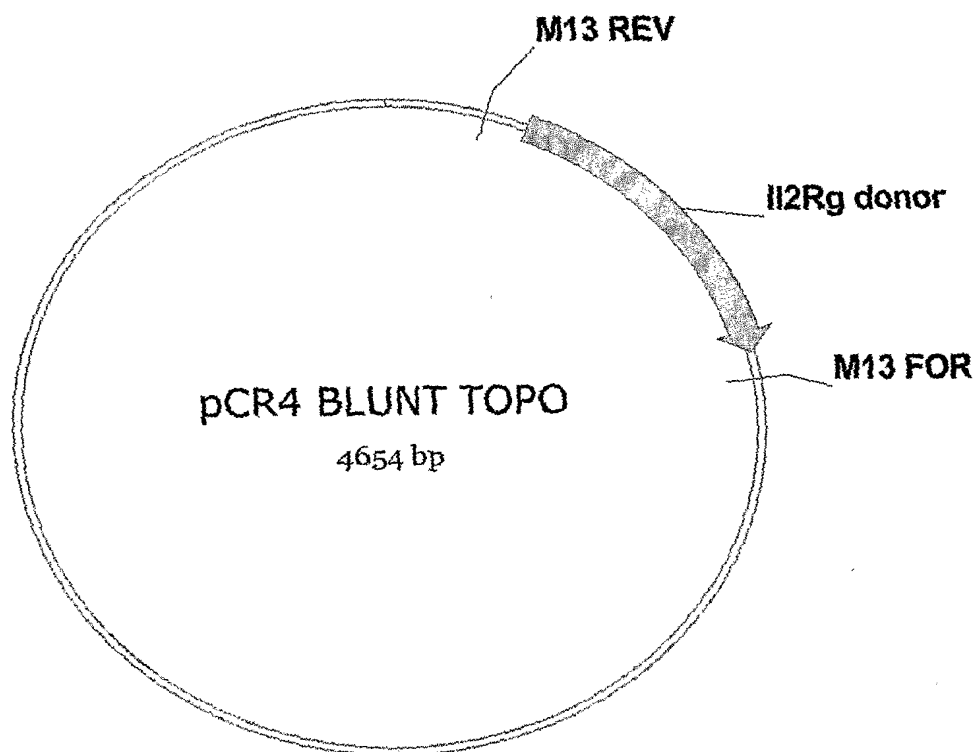


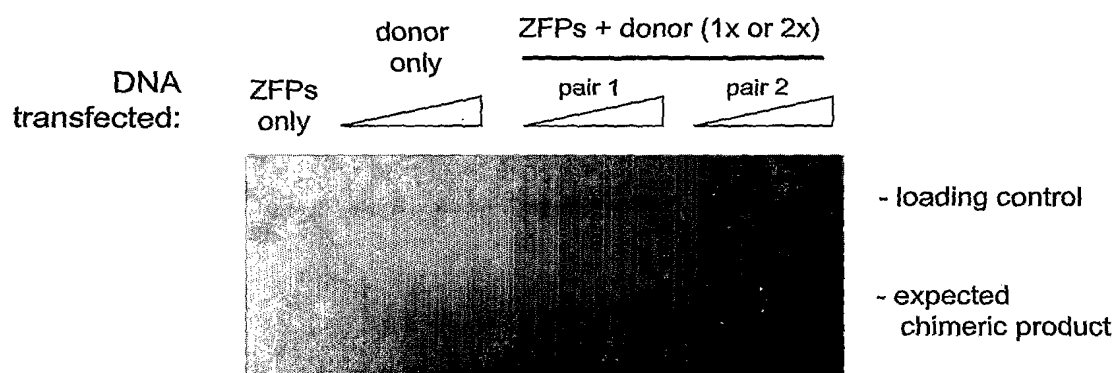
## FIGURE 9



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# FIGURE 10



**FIGURE 11**

## FIGURE 12

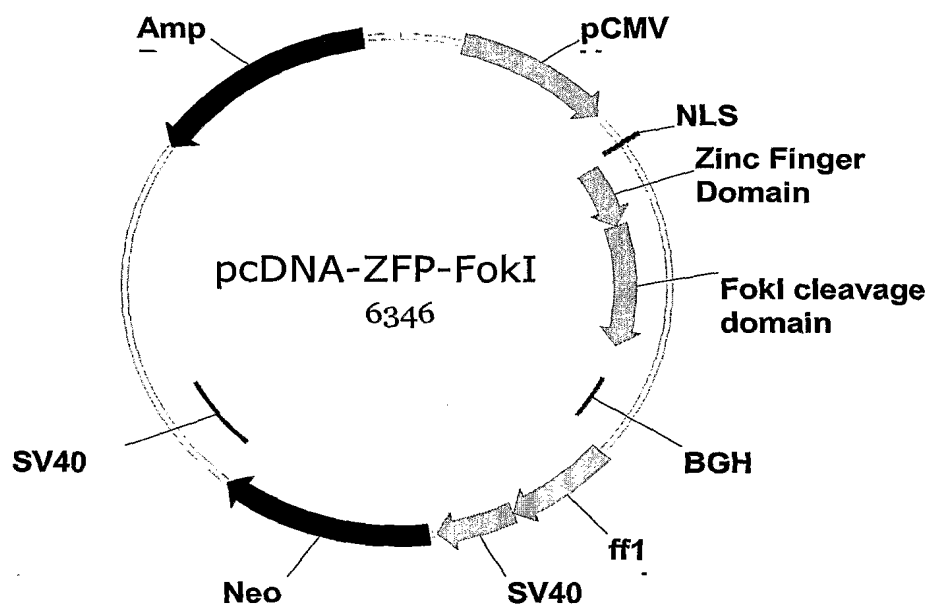
<u>TAGTCCTGCAGGTTTAAACGAATTGCGCCCTTTCCTCTAGGTAaAAGAA</u> <u>tT</u>	50
<u>CcGAcAAcGATAAAGTCCAGAAGTGCAGCCACTATCTATTCCCTGAAGAA</u>	100
ATCACTTCTGGCTGTCAGTTGCAAAAAAAGGAGATCCACCTCTACCAAAC	150
ATTTGTTGTTTCAGCTCCAGGACCCACGGGAACCCAGGAGACAGGCCACAC	200
AGATGCTAAAACTGCAGAATCTGGGTAATTTGGAAAGAAAGGGTCAAGAG	250
ACCAGGGATACTGTGGGACATTGGAGTCTACAGAGTAGTGTTCTTTTATC	300
ATAAGGGTACATGGGCAGAAAAGAGGAGGTAGGGGATCATGATGGGAAGG	350
GAGGAGGTATTAGGGGCACTACCTTCAGGATCCTGACTTGTCTAGGCCAG	400
GGGAATGACCACATATGCACACATATCTCCAGTGATCCCCTGGGCTCCAG	450
AGAACCTAACACTTCACAACTGAGTGAATCCCAGCTAGAACTGAACTGG	500
AACAACAGATTCTTGAACCACTGTTTGGAGCACTTGGTGCAGTACCGGAC	550
<u>TAAGGGCGAATTGCGGGCCGCTAAATTCAATTCGCCCTATAGTGAGTCGT</u>	600
<u>ATTACAATTCACTGGCCGTCGTTT</u>	

(SEQ ID NO:12)

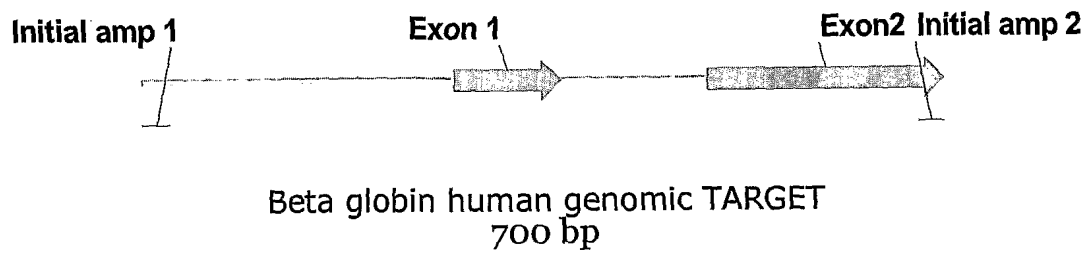
**FIGURE 13**

TACTGATGGTATGGGGCCAAGAGATATATCTTAGAGGGAGGGCTGAGGGT	50
TTGAAGTCCAACCTCCTAAGCCAGTGCCAGAAGAGCCAAGGACAGGTACGG	100
CTGTCATCACTTAGACCTCACCCCTGTGGAGCCACACCCTAGGGTTGGCCA	150
ATCTACTCCCAGGAGCAGGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGT	200
CAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGACACAACCTGTGTTC	250
ACTAGCAACCTCAAACAGACACCATGGTGCATCTGACTCCTGAGGAGAAG	300
TCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGG	350
TGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA	400
CCAATAGAACTGGGCATGTGGAGACAGAGAAGACTCTTGGGTTTCTGAT	450
AGGCACTGACTCTCTCTGCCTATTGGTCTATTTTCCCACCCTTAGGCTGC	500
TGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTG	550
TCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAA	600
GAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCA	650
AGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTG	700

(SEQ ID NO:13)

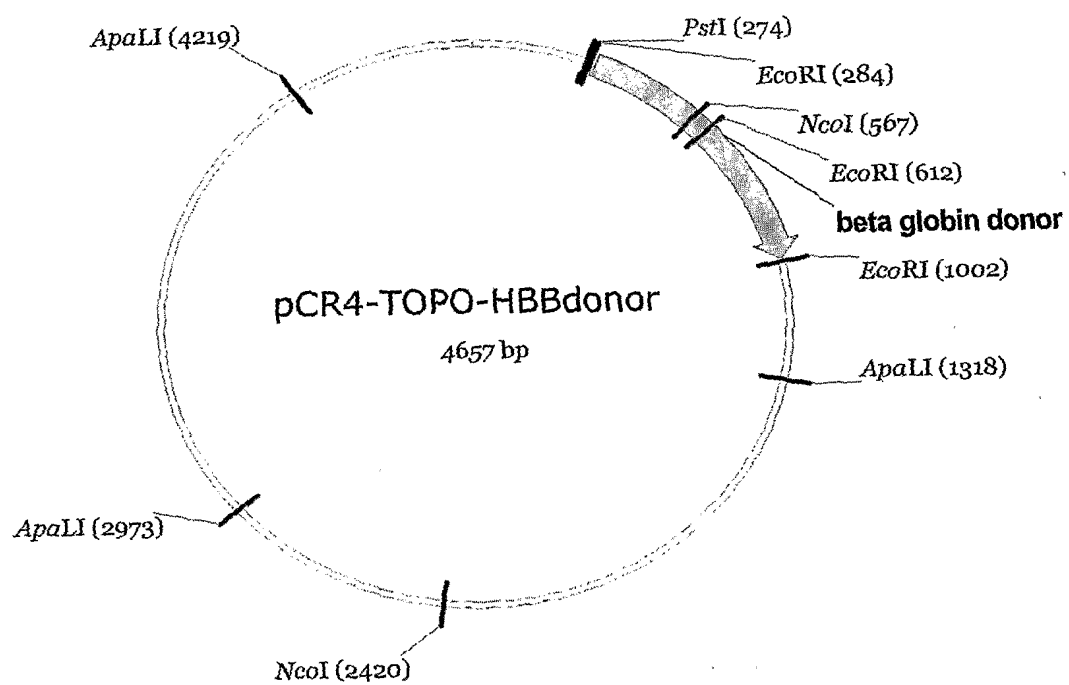
**FIGURE 14**

## FIGURE 15



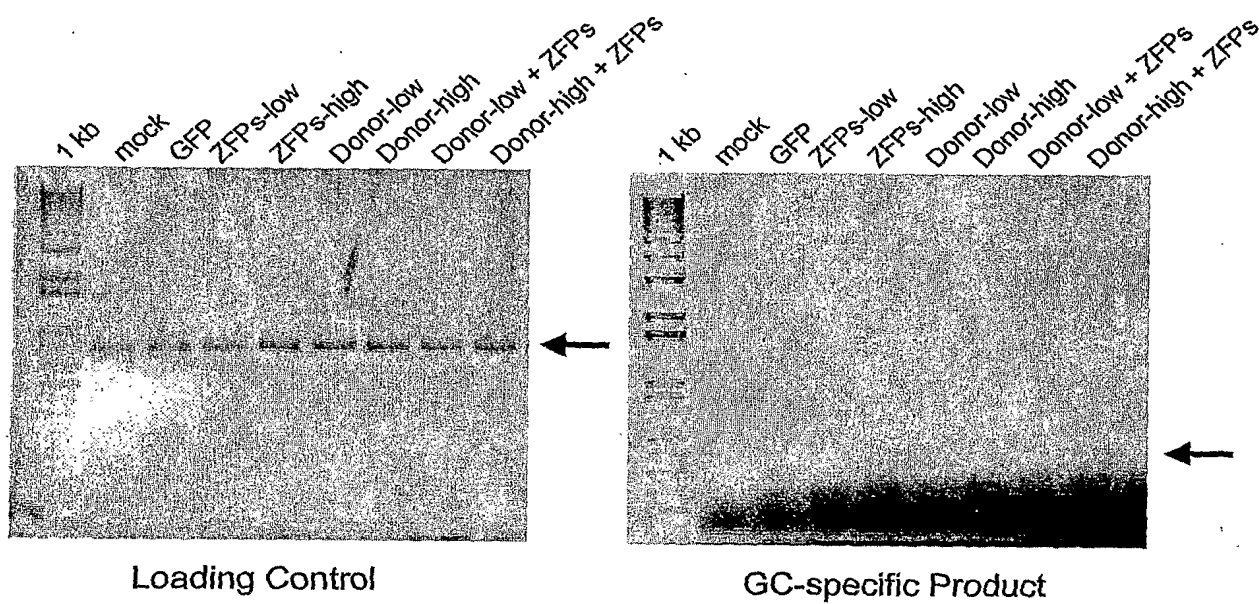
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## FIGURE 16





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**FIGURE 17**

**FIGURE 18**

<u>TGCTTACCAAGCTGTGATTCCAAATATTACGTAAATACACTTGCAAAGGA</u>	50
<u>GGATGTTTTTAGTAGCAATTTGTACTGATGGTATGGGGCCAAGAGATATA</u>	100
<u>TCTTAGAGGGAGGGCTGAGGGTTTGAAGTCCAACCTCCTAAGCCAGTGCCA</u>	150
<u>GAAGAGCCAAGGACAGGTACGGCTGTCATCACTTAGACCTCACCCTGTGG</u>	200
<u>AGCCACACCCTAGGGTTGGCCAATCTACTCCCAGGAGCAGGGAGGGCAGG</u>	250
<u>AGCCAGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATT</u>	300
<u>TGCTTCTGACACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGT</u>	350
<u>GCATCTGACTCCTGAGGAGAAGTCTGgCGTTAgTGCCCgaattccgAtcG</u>	400
<u>TcAACcac</u>	

(SEQ ID NO:14)

## FIGURE 19

5-8  
CACGTTTCGTGTTTCGGAGCCGCTTTAACCCACTCTGTGGAAG  
GTGCAAAGCACAAGCCTCGGCGAAATTGGGTGAGACACCTTC  
5-10

(SEQ ID NO:15)

**FIGURE 20**

```
1  MAPKKKRVG  IHGVPAAAE  RPFQCRICMR  NFSRSDNLSE  HIRHTTGEKP  FACDICGRKF
61  ARNAHRLNHT  KIHTGSQKPF  QCRICMRNFS  RSDTLSEHIR  THTGEKPFAC  DICGRKFAAR
121  STRTTHTKIH  LRQKDAARGS  QLVKSELEEK  KSELRHKLKY  VPHEYIELIE  IARNSTQDRI
181  LEMKVMEFFM  KVYGYRGKHL  GGSRKPDGAI  YTVGSPIDYG  VIVDTKAYSG  GYNLPIGQAD
241  EMQRYVEENQ  TRNKHINPNE  WWKVYPSSVT  EPKFLFVSGH  FKGNYKAQLT  RLNHITNCNG
301  AVLSVEELLI  GGEMIKAGTL  TLEEVRRKFN  NGEINF
```

(SEQ ID NO:16)

**FIGURE 21**

1	<u>MAPKKKRVG</u>	<u>IHGVPAAAE</u>	RPFQCRICMR	NFSRSDSLSR	HIRTHTGEKP	FACDICGRKF
61	<u>ADSSNRKTH</u>	<u>TIHTGGGGSQ</u>	KPFQCRICMR	NFSRSDSLSV	HIRTHTGEKP	FACDICGRKF
121	<u>ADRSNRITHT</u>	<u>KIHLRQKDA</u>	<u>RGSQLVKSEL</u>	EEKKSELRHK	LKYVPHEYIE	LIEIARNSTQ
181	DRILEMKVME	FFMKVYGYRG	KHLGGSRKPD	GAIYTVGSPI	DYGVIVDTKA	YSGGYNLPIG
241	<u>QADEMQRYVE</u>	ENQTRNKHIN	PNEWWKVYPS	SVTEFKFLFV	SGHPKGNKYA	QLTRLNHITN
301	CNGAVLSVEE	LLIGGEMIKA	GTLTLEEVRR	KFNNGEINF		

(SEQ ID NO:17)

**FIGURE 22**

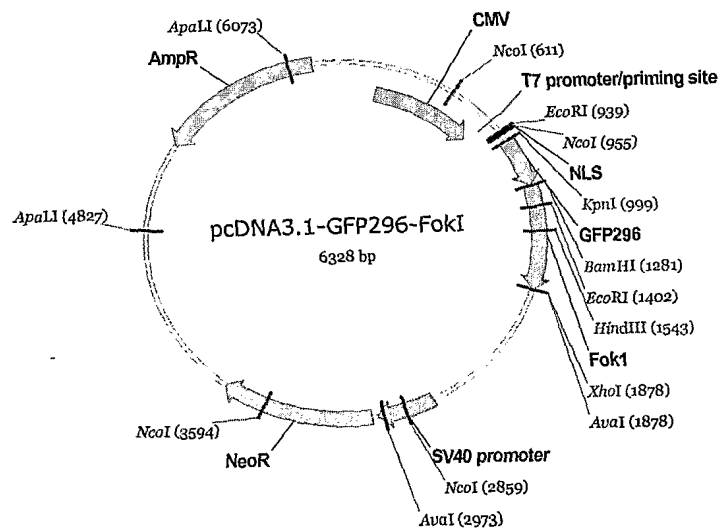
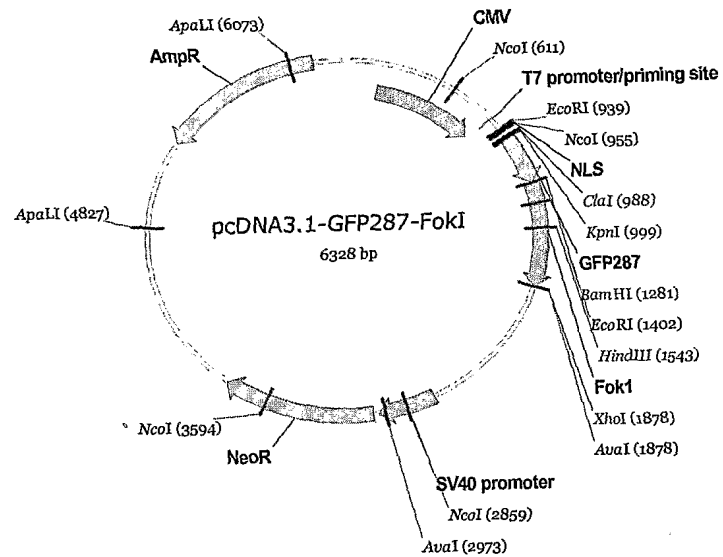
CGAATTCTGCAGTCGACGGTACCGCGGGCCCCGGGATCCACCGGTCGCCACCATGGTGAGC  
AAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA  
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG  
ACCCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCCCACCCCTCGTGACC  
ACCCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCCGACCACATGAAGCAGCACGAC  
TTCTTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC  
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGC  
ATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAG  
TACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAG  
GTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTAC  
CAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGC  
ACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG  
TTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGC  
GACTCTAGATCATAATC

(SEQ ID NO:18)

**FIGURE 23**

CGAATTCTGCAGTCGACGGTACCGCGGGCCCCGGGATCCACCGGTCGCCACCATGGTGAGC  
AAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA  
AACGGCCACAAGTTCAGCGTGTCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG  
ACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACC  
ACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCTAACACGAAGCAGCAGGACTT  
CTTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGA  
CGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCAT  
CGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTA  
CAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGT  
GAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCA  
GCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCAC  
CCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTT  
CGTGACCGCCCGCGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCGA  
CTCTAGATCATAATC

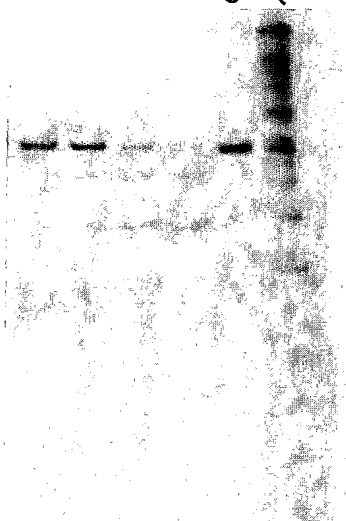
(SEQ ID NO:19)

**FIGURE 24**

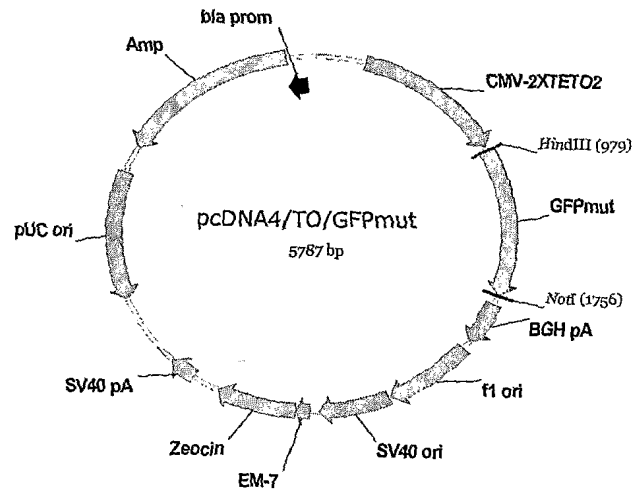


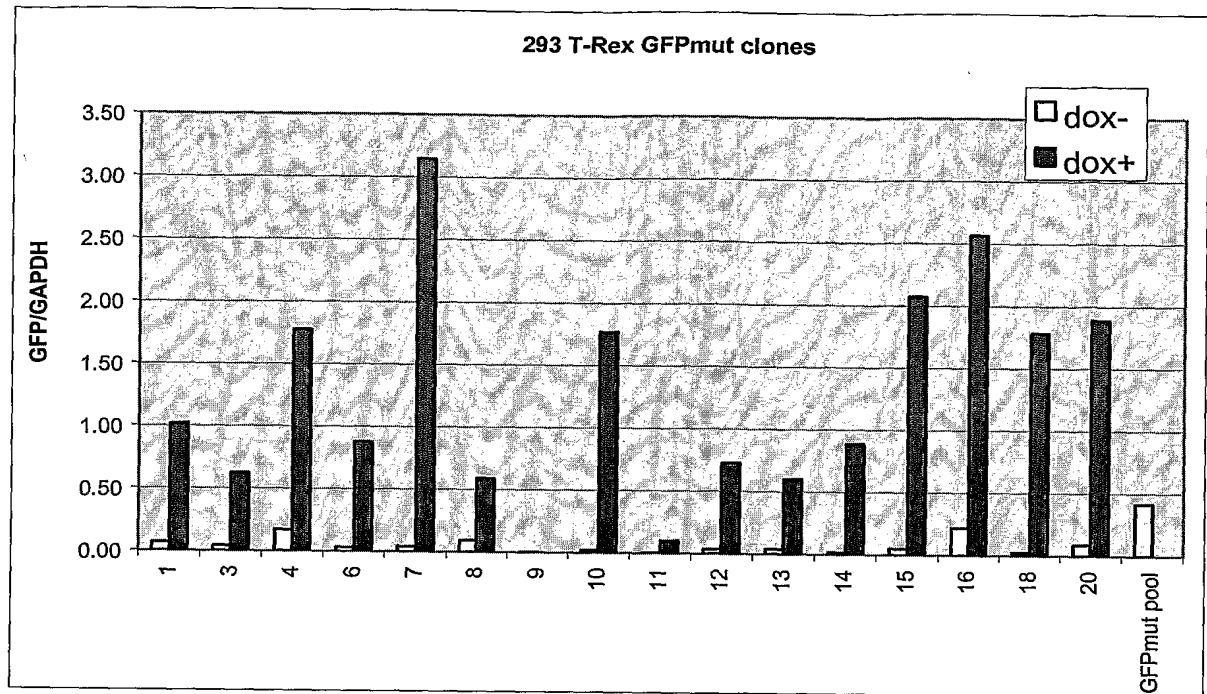
# FIGURE 25

287a-F1/296s-F1  
Uncut control  
Marker

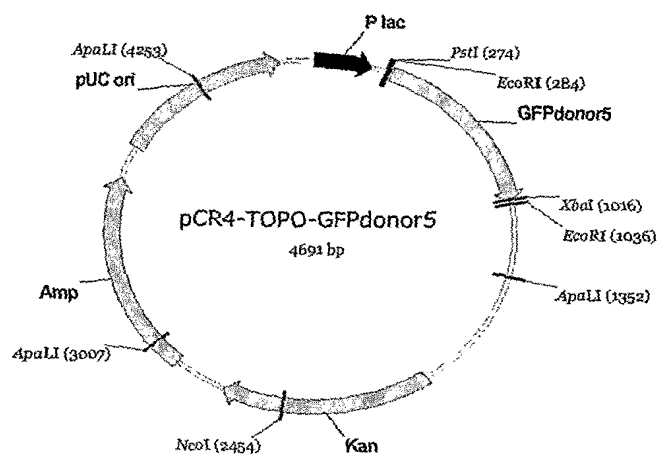


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**FIGURE 26**

**FIGURE 27**

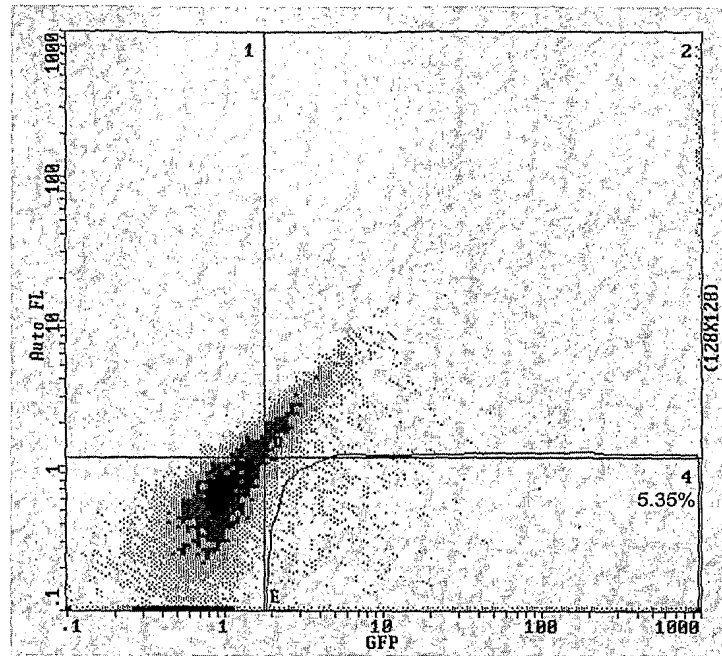
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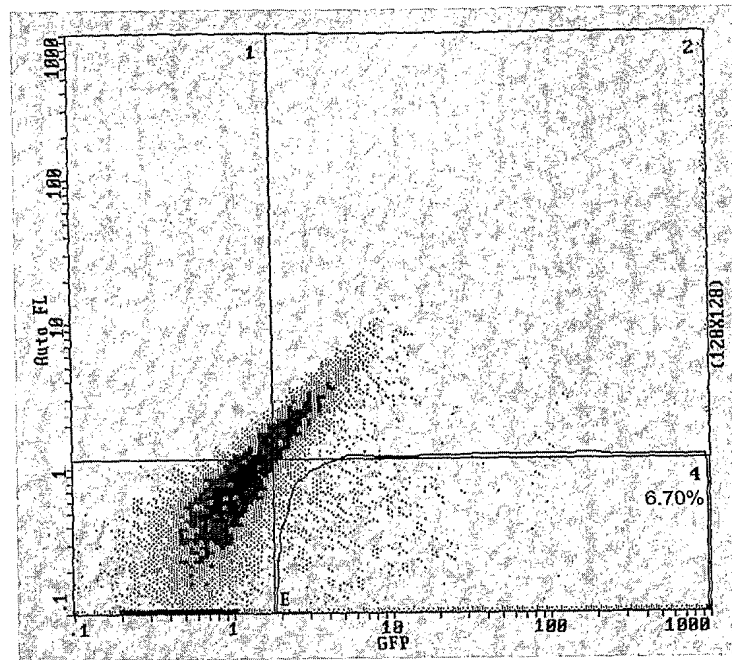
**FIGURE 28**

**FIGURE 29**

GGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAAC  
GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACC  
CTGAAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCCACCCTCGTGACCACC  
CTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTC  
TTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGAC  
GGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC  
GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTAC  
AACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTG  
AACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCCTACCAG  
CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCCTACCTGAGCACC  
CAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTC  
GTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCGAC  
TCTAGATCATAATC

(SEQ ID NO:20)

**FIGURE 30**

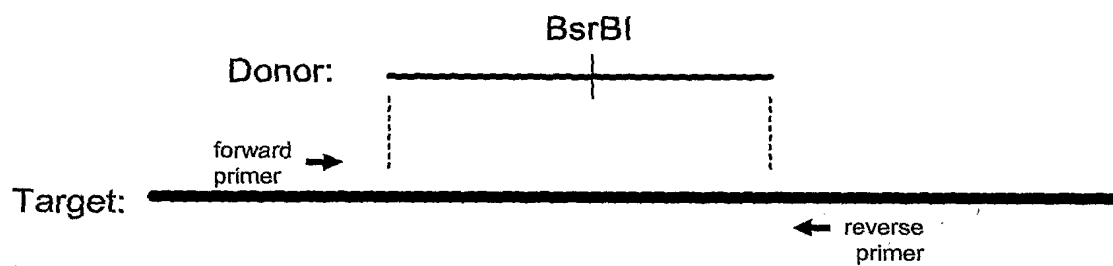
**FIGURE 31**

**FIGURE 32**

GGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAAC  
GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACC  
CTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACC  
CTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGGACTTC  
TTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGAC  
GGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC  
GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTAC  
AACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTG  
AACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAG  
CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACC  
CAGTCCGCCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCCTGCTGGAGTTC  
GTGACCGCCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCTCG  
AGTCTAGAGGGCCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGC  
CATCTGTTGTTTGGCCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACCTG  
TCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCAATTCTATTC  
TGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATG  
CTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGG  
GGTATCCCCACGCGCCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCA  
GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTCTTCCCTTCCT  
TTCTCGCCACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT  
TCCGATTTAGTGCTTTACGGCACCTCGACCCCCAAAAAAGTTGATTAGGGTGATGGTTTAC  
GTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCT  
TTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTT  
TTGATTTATAAGGGATTTTGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAAC  
AAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCC  
AGGCTCCCCAGCAGGCAGAAGTATGCA

(SEQ ID NO:21)



**FIGURE 33**

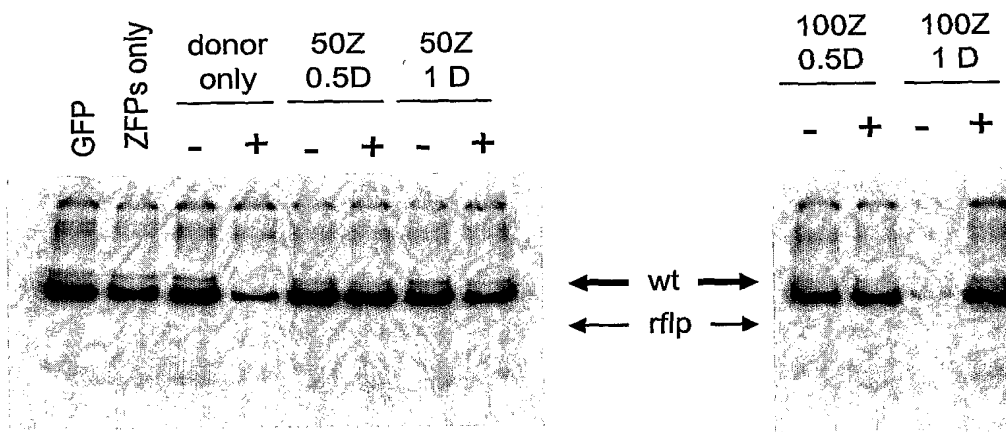
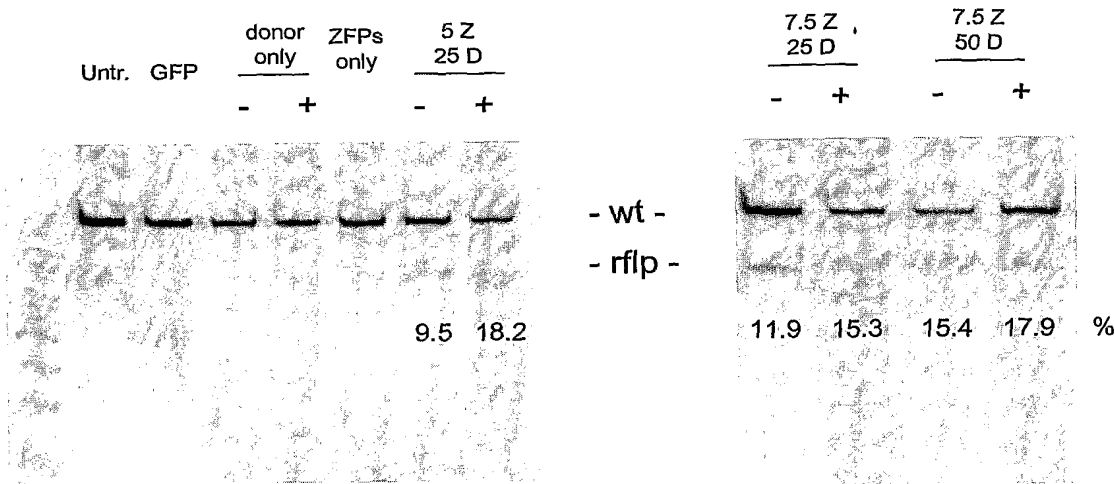
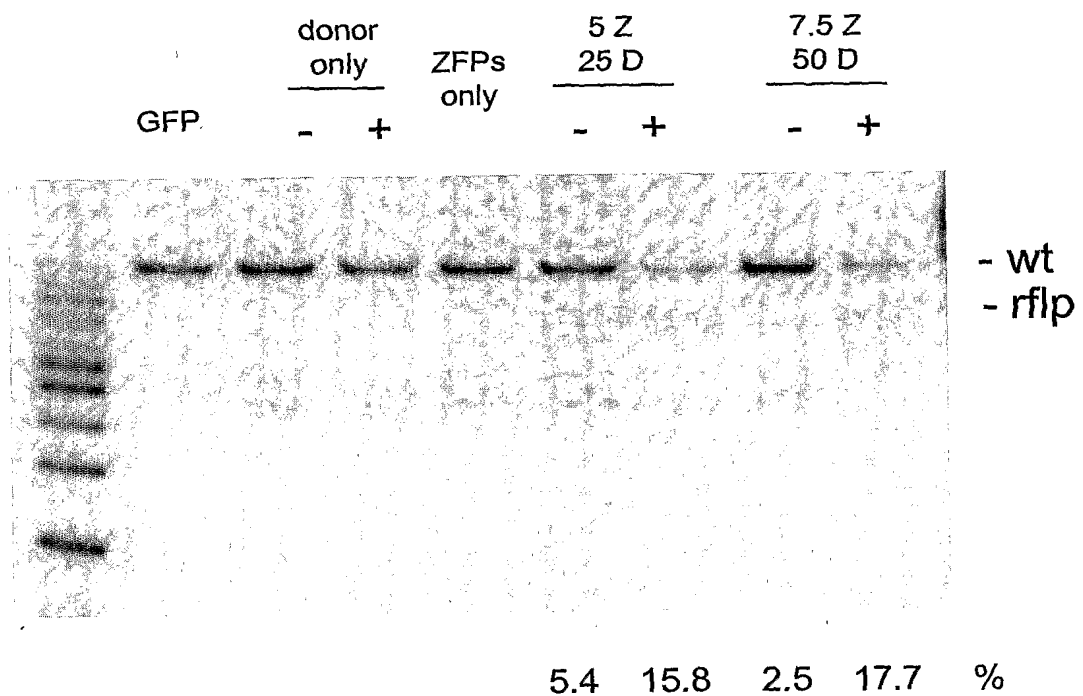
**FIGURE 34**

FIGURE 35



**FIGURE 36**



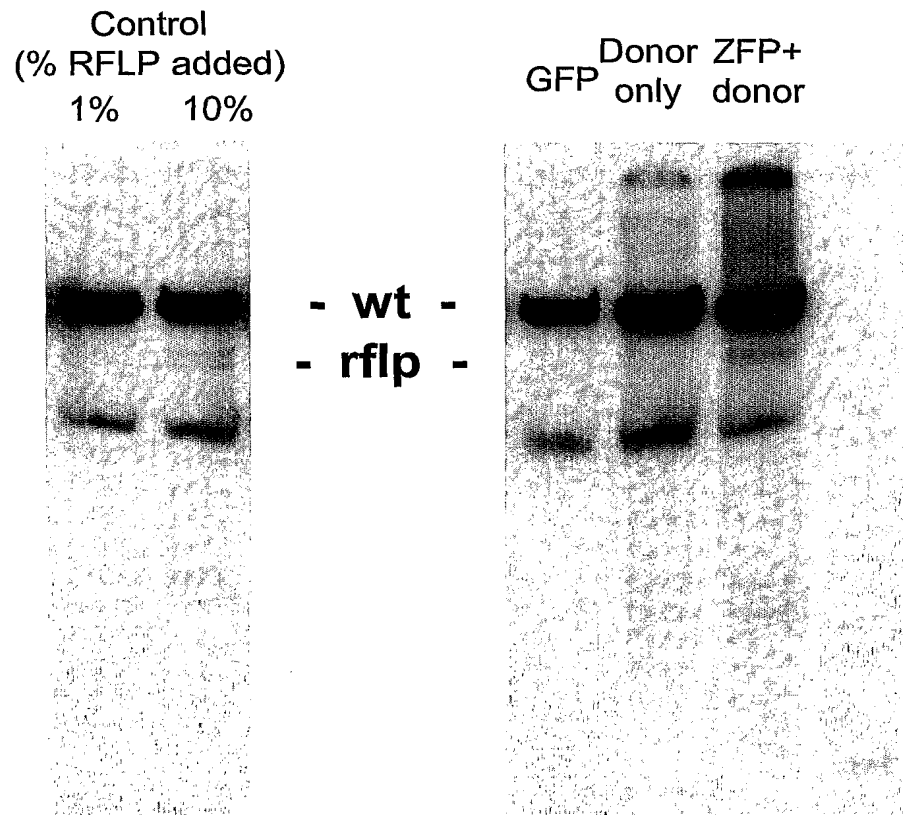
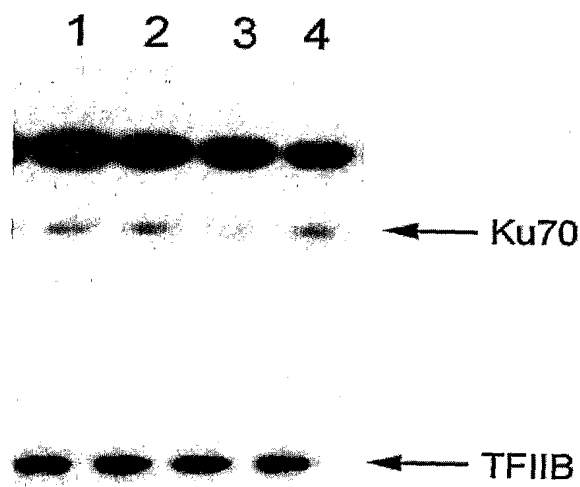
**FIGURE 38**

FIGURE 39



**FIGURE 40****sca-29b:**

MAERPFQCRICMRNFSQSGDLTRHIRTHTGEKPFACDICGRKFATSANLSRHTK  
IHTGGGGSQKPFQCRICMRNFSDRSALSRHIRTHTGEKPFACDICGRKFAQSG  
HLSRHTKIH (SEQ ID NO:22)

**sca-36a:**

MAERPFQCRICMRNFSRSQTRKTHIRTHTGEKPFACDICGRKFAQKRNRTKHT  
KIHTGSQKPFQCRICMRNFSDRSALSRHIRTHTGEKPFACDICGRKFAQSGNLA  
RHTKIH (SEQ ID NO:23)

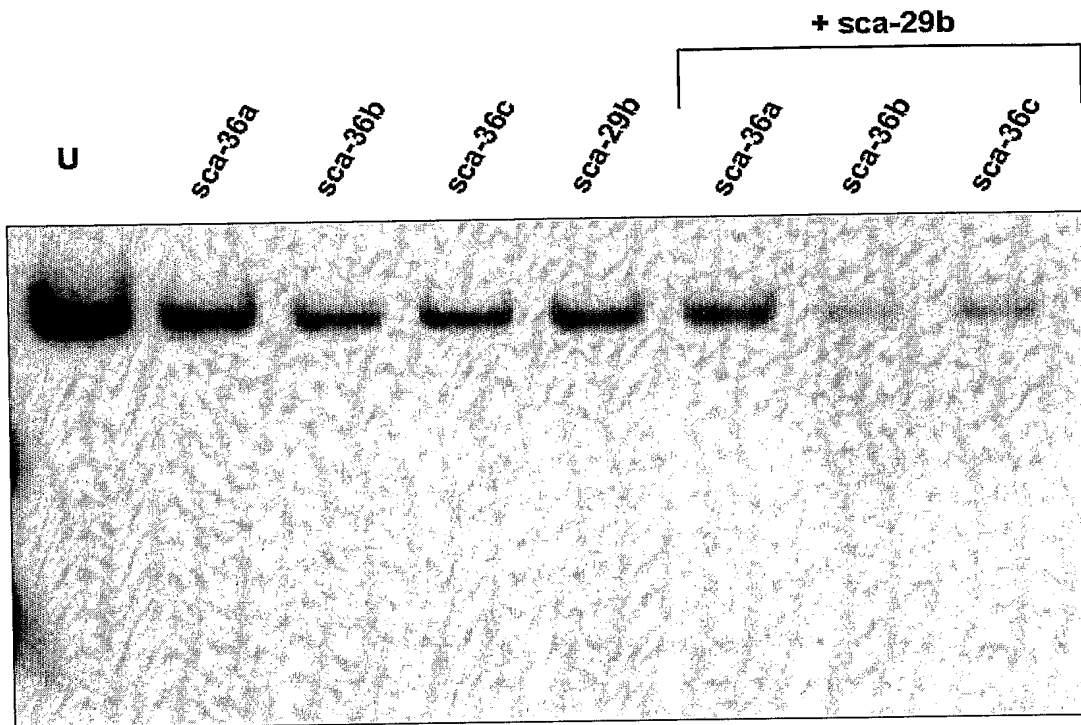
**sca-36b:**

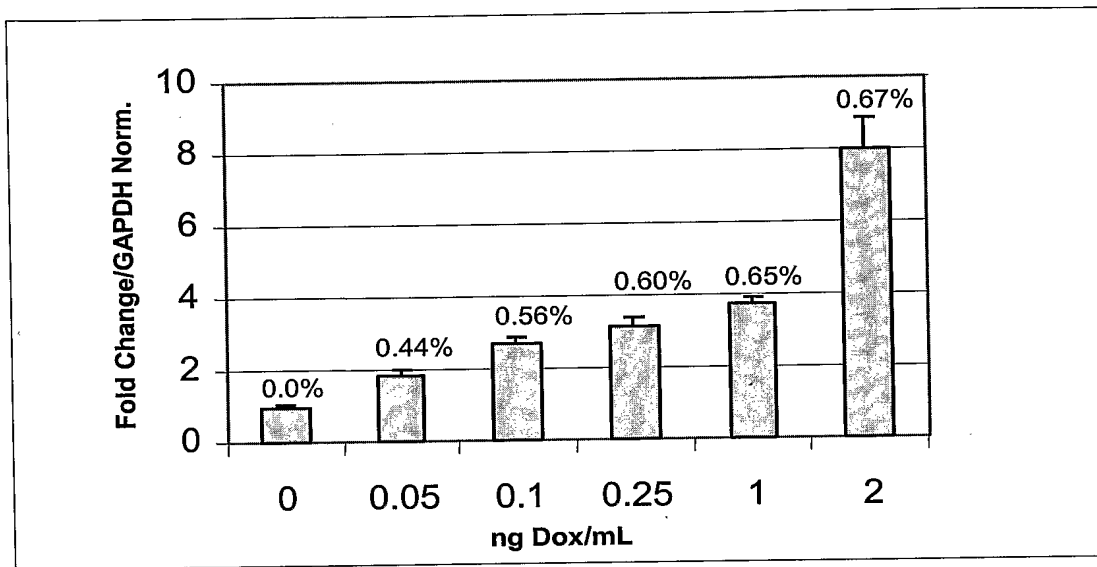
MAERPFQCRICMRNFSTSGSLSRHIRTHTGEKPFACDICGRKFADRSDLSRHTK  
IHTGGGGSQKPFQCRICMRNFSDRSALSRHIRTHTGEKPFACDICGRKFAQSG  
NLARHTKIH (SEQ ID NO:24)

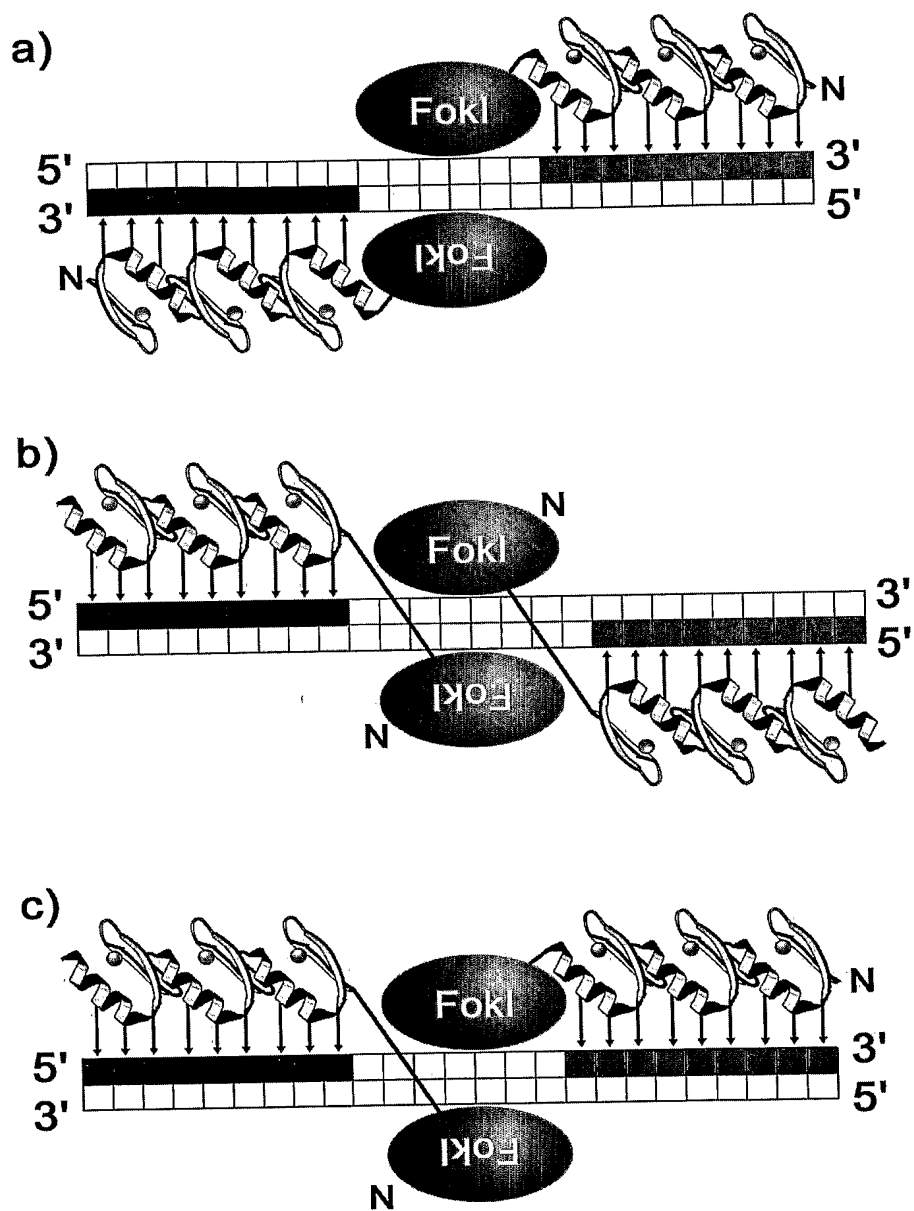
**sca-36c:**

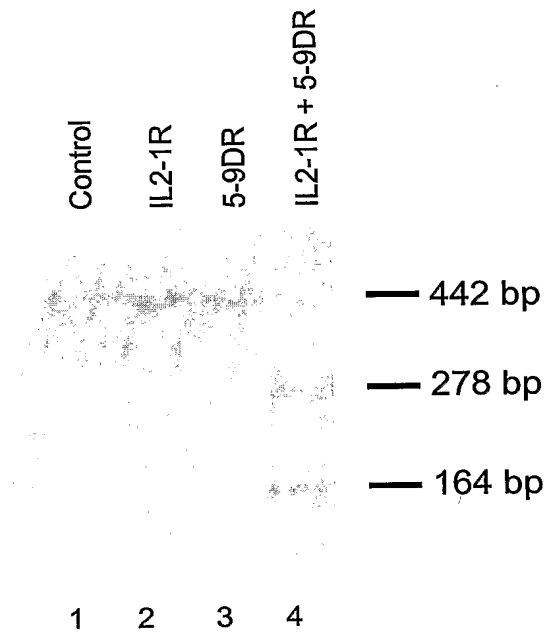
MAERPFQCRICMRNFSTSSSLSRHIRTHTGEKPFACDICGRKFADRSDLSRHTK  
IHTGGGGSQKPFQCRICMRNFSDRSALSRHIRTHTGEKPFACDICGRKFAQSG  
NLARHTKIH (SEQ ID NO:25)



**FIGURE 41**

**FIGURE 42**

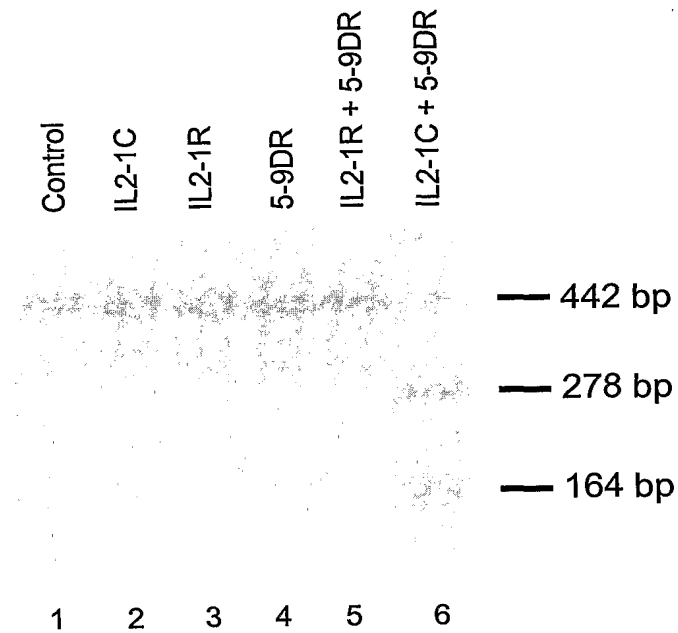
**FIGURE 43**

**FIGURE 44**

**59D**  
-tAAAGCGGCTCCGaaccacATTATCCGAGTTc-  
-aTTTCGCCGAGGcttggtgTAATAGGCTCAAg-  
**IL2-1**

(SEQ ID NO: 211)

## FIGURE 45



59D IL2-1

-tAAAGCGGCTCCGaaccacAACTCGGATAATg-

-aTTTCGCCGAGGcttggtgTTGAGCCTATTac-

(SEQ ID NO: 212)